

Report Documentation Page			Form Approved OMB No. 0704-0188	
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1. REPORT DATE AUG 2010	2. REPORT TYPE	3. DATES COVERED 00-00-2010 to 00-00-2010		
4. TITLE AND SUBTITLE High-Redundancy Draft Sequencing of 15 Clinical and Environmental Burkholderia Strains			5a. CONTRACT NUMBER	
			5b. GRANT NUMBER	
			5c. PROGRAM ELEMENT NUMBER	
6. AUTHOR(S)			5d. PROJECT NUMBER	
			5e. TASK NUMBER	
			5f. WORK UNIT NUMBER	
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) Naval Medical Research Center, Biological Defense Research Directorate, Silver Spring, MD, 20910			8. PERFORMING ORGANIZATION REPORT NUMBER	
9. SPONSORING/MONITORING AGENCY NAME(S) AND ADDRESS(ES)			10. SPONSOR/MONITOR'S ACRONYM(S)	
			11. SPONSOR/MONITOR'S REPORT NUMBER(S)	
12. DISTRIBUTION/AVAILABILITY STATEMENT Approved for public release; distribution unlimited				
13. SUPPLEMENTARY NOTES				
14. ABSTRACT				
15. SUBJECT TERMS				
16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT Same as Report (SAR)	18. NUMBER OF PAGES 2
a. REPORT unclassified	b. ABSTRACT unclassified	c. THIS PAGE unclassified		

GENOME ANNOUNCEMENTS

High-Redundancy Draft Sequencing of 15 Clinical and Environmental *Burkholderia* Strains[▽]

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Received 20 August 2010/Accepted 30 August 2010

The Gram-negative *Burkholderia* genus includes several species of intracellular bacterial pathogens that pose substantial risk to humans. In this study, we have generated draft genome sequences of 15 strains of *B. oklahomensis*, *B. pseudomallei*, *B. thailandensis*, and *B. ubonensis* to an average sequence read coverage of 25- to 40-fold.

The Gram-negative *Burkholderia* genus includes several species of intracellular bacterial pathogens that pose substantial risk to humans. The high virulence of the *B. pseudomallei/B. mallei* species by the respiratory route and the fact that the bacteria can be aerosolized has caused them to be considered biothreats (1); both *B. pseudomallei* and *B. mallei* have been designated category B select agents by the Centers for Disease Control and Prevention (CDC) (18).

Genomes of 15 strains of *B. oklahomensis*, *B. pseudomallei*, *B. thailandensis*, and *B. ubonensis* were sequenced using the Roche/454 Sequencing GS-20 instrument (13). The average read length obtained from the 15 libraries was 97 nucleotides (nt). Raw sequence data assembled into 450 to 1,000 contigs of more than 1,000 nt per genome, with an average redundancy of coverage of 25 to 40 reads per base. The GC contents of the nucleotide sequences of the strains were 63 to 67%.

High-redundancy draft genome sequencing is an economic way of assessing species diversity and is used to screen strains for subsequent genome sequence completion. The data generated in this project have already proved useful in helping to

identify conserved vaccine targets (2), have been incorporated into global comparative genomics analyses of the *Burkholderia* genus (16, 20), and have been used for identification of candidate loci for multilocus variable-number tandem-repeat typing schemes (19).

Brief strain descriptions. *B. pseudomallei* strain B7210 is a human isolate from Australia, obtained in a case of empyema infection in 1970 (4, 6). Strain BCC 215 is an isolate obtained in a fatal case of septicemic melioidosis in a family located in rural northeastern Brazil. Three of four affected children, all siblings, died. An indirect hemagglutination assay (IHA) indicated seroconversion subsequent to clinical recovery for the one survivor (17). DM98, a strain with a persistently mucoid phenotype, was isolated in a single case of septicemic melioidosis in tropical northern Australia and was obtained from a blood culture (8). NCTC 13177 (also known as BCC 6) was isolated in an outbreak of fatal septicemic melioidosis cases in northwestern Australia that were linked to a contaminated water supply (9–11). PHLS 9 (CDC2002721637) is a human isolate from Pakistan, obtained in 1988 (4, 6). PHLS 14 was isolated from a monkey liver in the Philippines in 1990 (4, 6). PHLS 91 is a sheep lung isolate from Australia, obtained in 1984 (4, 6). PHLS 112 is a human isolate obtained from northeast Thailand in 1992 (4, 6). Strain 7894 is a human isolate obtained from Ecuador in 1962 (4, 6).

B. oklahomensis strain C6786 was isolated from an infected human in Oklahoma (7, 14). E0147 was isolated in a case of human infection in Georgia (7, 15).

B. thailandensis Bt4 is an environmental isolate from northern Australia, obtained during an investigation of *Burkholderia* ecology in potable water supply systems (12). MSMB43 is an arabinose-assimilating environmental strain from a borehole near Darwin, Northern Territories, Australia, and falls into an intermediate phylogenetic clade relative to *B. pseudomallei* and

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▽ Published ahead of print on 24 September 2010.

B. thailandensis (3). CDC3015869 (TXDOH) was isolated from the blood of a 2-year-old boy infected after a near-drowning incident (5).

B. ubonensis strain Bu was isolated from a rhizosphere sample from a mine site in northern Australia (12).

Nucleotide sequence accession numbers. The sequences determined in this study have been deposited in the National Center for Biotechnology Information (NCBI) RefSeq database under the following accession numbers: for *B. pseudomallei* strains B7210, BCC 215, DM98, NCTC 13177, PHLS 9, PHLS 14, PHLS 91, PHLS 112, and 7894, NZ_ABBN00000000, NZ_ABBR00000000, NZ_ABBI00000000, NZ_ABBQ00000000, NZ_ABBL00000000, NZ_ABBJ00000000, NZ_ABBK00000000, NZ_ABBP00000000, and NZ_ABBO 00000000, respectively; for *B. oklahomensis* strains C6786 and E0147, NZ_ABBG00000000 and NZ_ABBF00000000; for *B. thailandensis* strains Bt4, MSMB43, and CDC3015869, NZ_ABBH00000000, NZ_ABBM00000000, and NZ_ABBD00000000, respectively; and for *B. ubonensis* strain Bu, NZ_ABBe00000000.

We thank Patricia Wilkins, Alex Hoffmaster, David Ussery, and Peter Hallin for their help with this study.

This work was funded by grant XX0013_06_NM_B from the Defense Threat Reduction Agency to T.D.R. Some of the authors are employees of the U.S. Government, and this work was prepared as part of their official duties.

The views expressed in this article are those of the authors and do not necessarily reflect the official policy or position of the U.S. Department of the Navy, U.S. Department of Defense, U.S. Centers for Disease Control and Prevention, U.S. Department of Health and Human Services, or U.S. Government.

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